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- b) determining whether the activity of the polypeptide is reduced or increased by the chemical compound and, where appropriate, and
 - c) determining the compound which specifically reduces or increases the activity of the polypeptide.

17. (Amended) A method for finding a compound which alters the expression of polypeptides with the biological activity of a very long chain fatty acid elongase, comprising the steps of:

- a) contacting a host cell containing a nucleic acid coding for a polypeptide with the biological activity of a very long chain fatty acid elongase with a chemical compound or a mixture of chemical compounds,
- b) determining the polypeptide concentration, and
- c) determining the compound which specifically influences the expression of the polypeptide.

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20. (Amended) A modulator of VLCFAE which are found by a method according to Claim 16.

21. (Amended) A herbicidally active substance found by a method according to Claim 16.

23. (Amended) An plant item selected from the group consisting of transgenic plants, parts of plants, protoplasts, plant tissues and plant propagation materials, comprising an introduced nucleic acid coding for a polypeptide having SEQ ID NO: 2, wherein the intracellular concentration of a polypeptide according to Claim 14 is increased or reduced compared with the corresponding wild-type cells.

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24. (Amended) An plant item selected from the group consisting of plants, parts of plants, protoplasts, plant tissues or plant propagation materials, comprising a polypeptide having SEQ ID NO: 2 whose biological

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activity or expression pattern is altered by comparison with the corresponding endogenous polypeptides.

Please add the following claims:

--25. A modulator of VLCFAE which are found by a method according to Claim 17.

26. A herbicidally active substance found by a method according to Claim 17.

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27. A method according to Claim 15, wherein the polypeptide comprises a sequence selected from the group consisting of:

- a) the sequence shown in SEQ ID NO: 2,
- b) sequences encoded by a nucleic acid having SEQ ID NO: 1,
- c) partial sequences of the sequences defined under a) or b) which still have the biological activity of a VLCFAE,
- d) sequences which have an identity of at least 60% with the sequences defined under a) to c),
- e) sequences which include the C-terminally localized active site of the polypeptide shown in SEQ ID NO: 2,
- f) sequences which have an identity of at least 60% with the sequences defined under e),
- g) sequences which include the specific N terminus of the polypeptide shown in SEQ ID NO: 2,
- h) sequences which have an identity of at least 60% with the sequences defined under g).

28. A method according to Claim 15, wherein the polypeptide comprises a sequence selected from the group consisting of:

- a) the sequence shown in SEQ ID NO: 2,
- b) sequences encoded by a nucleic acid having SEQ ID NO: 1,
- c) sequences which include the C-terminally localized active site of

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- d) sequences which include the specific N terminus of the polypeptide shown in SEQ ID NO: 2,
29. A method according to Claim 16, wherein the polypeptide comprises a sequence selected from the group consisting of:
- the sequence shown in SEQ ID NO: 2,
 - sequences encoded by a nucleic acid having SEQ ID NO: 1,
 - partial sequences of the sequences defined under a) or b) which still have the biological activity of a VLCFAE,
 - sequences which have an identity of at least 60% with the sequences defined under a) to c),
 - sequences which include the C-terminally localized active site of the polypeptide shown in SEQ ID NO: 2,
 - sequences which have an identity of at least 60% with the sequences defined under e),
 - sequences which include the specific N terminus of the polypeptide shown in SEQ ID NO: 2, and
 - sequences which have an identity of at least 60% with the sequences defined under g).
30. A method according to Claim 16, wherein the polypeptide comprises a sequence selected from the group consisting of:
- the sequence shown in SEQ ID NO: 2,
 - sequences encoded by a nucleic acid having SEQ ID NO: 1,
 - sequences which include the C-terminally localized active site of the polypeptide shown in SEQ ID NO: 2, and
 - sequences which include the specific N terminus of the polypeptide shown in SEQ ID NO: 2.
31. A method according to Claim 17, nucleic acid comprises a sequence selected from the group consisting of:
- the sequence shown in SEQ ID NO: 1,
 - sequences which code for a polypeptide comprising the amino acid sequence shown in SEQ ID NO: 2,

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- c) partial sequences at least 14 base-pairs long of the sequences defined under a) or b),
 - d) sequences which hybridize to the sequences defined under a) or b),
 - e) sequences which have an identity of at least 60% with the sequences defined under a) or b),
 - f) sequences which code for the C-terminally localized active site of the polypeptide shown in SEQ ID NO: 2
 - g) sequences which have an identity of at least 60% with the sequences defined under f),
 - h) sequences which code for the specific N terminus of the polypeptide shown in SEQ ID NO: 2,
 - i) sequences which have an identity of at least 60% with the sequences defined under h),
 - j) sequences which are complementary to the sequences defined under a) to i), and
 - k) sequences which, because of the degeneracy of the genetic code, code for the same amino acid sequence as the sequences defined under a) to h).

32. A method according to Claim 17, nucleic acid comprises a sequence selected from the group consisting of:

- a) the sequence shown in SEQ ID NO: 1,
 - b) sequences which code for a polypeptide comprising the amino acid sequence shown in SEQ ID NO: 2,
 - c) sequences which hybridize to the sequences defined under a) or b),
 - d) sequences which code for the C-terminally localized active site of the polypeptide shown in SEQ ID NO: 2
 - e) sequences which code for the specific N terminus of the polypeptide shown in SEQ ID NO: 2,
 - f) sequences which are complementary to the sequences defined under a) to e), and

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33. A transgenic plant comprising a nucleic acid comprises a sequence selected from the group consisting of:
- the sequence shown in SEQ ID NO: 1,
 - sequences which code for a polypeptide comprising the amino acid sequence shown in SEQ ID NO: 2,
 - sequences which code for the C-terminally localized active site of the polypeptide shown in SEQ ID NO: 2
 - sequences which code for the specific N terminus of the polypeptide shown in SEQ ID NO: 2,
 - sequences which are complementary to the sequences defined under a) to d), and
 - sequences which, because of the degeneracy of the genetic code, code for the same amino acid sequence as the sequences defined under a) to e).
34. A transgenic plant according to Claim 33, comprising a nucleic acid comprises a sequence selected from the group consisting of:
- the sequence shown in SEQ ID NO: 1, and
 - sequences which code for a polypeptide comprising the amino acid sequence shown in SEQ ID NO: 2.
35. A method of determining with a target compound binds to a nucleic acid sequence coding a very long chain fatty acid elongase, comprising the step of contacting the target compound with a nucleic acid comprising a sequence selected form the group consisting of:
- the sequence shown in SEQ ID NO: 1,
 - sequences which code for a polypeptide comprising the amino acid sequence shown in SEQ ID NO: 2,
 - partial sequences at least 14 base-pairs long of the sequences defined under a) or b)

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- d) sequences which hybridize to the sequences defined under a) or b),
 - e) sequences which have an identity of at least 60% with the sequences defined under a) or b),
 - f) sequences which code for the C-terminally localized active site of the polypeptide shown in SEQ ID NO: 2
 - g) sequences which have an identity of at least 60% with the sequences defined under f),
 - h) sequences which code for the specific N terminus of the polypeptide shown in SEQ ID NO: 2,
 - i) sequences which have an identity of at least 60% with the sequences defined under h),
 - j) sequences which are complementary to the sequences defined under a) to i), and
 - k) sequences which, because of the degeneracy of the genetic code, code for the same amino acid sequence as the sequences defined under a) to h).

36. A method according to Claim 35, wherein the nucleic acid comprising a sequence selected from the group consisting of:

- a) the sequence shown in SEQ ID NO: 1,
- b) sequences which code for a polypeptide comprising the amino acid sequence shown in SEQ ID NO: 2,
- c) sequences which hybridize to the sequences defined under a) or b),
- d) sequences which code for the C-terminally localized active site of the polypeptide shown in SEQ ID NO: 2,
- e) sequences which code for the specific N terminus of the polypeptide shown in SEQ ID NO: 2,
- f) sequences which are complementary to the sequences defined under a) to e), and
- g) sequences which, because of the degeneracy of the genetic code, code for the same amino acid sequence as the sequences defined under a) to h).

37. A method of determining whether a target compound binds to a very long chain fatty acid elongase polypeptide, comprising the step of contacting the target compound with a polypeptide comprising a sequence selected from the group consisting of:

- a) the sequence shown in SEQ ID NO: 2,
- b) sequences encoded by a nucleic acid having SEQ ID NO: 1,
- c) partial sequences of the sequences defined under a) or b) which still have the biological activity of a VLCFAE,
- d) sequences which have an identity of at least 60% with the sequences defined under a) to c),
- e) sequences which include the C-terminally localized active site of the polypeptide shown in SEQ ID NO: 2,
- f) sequences which have an identity of at least 60% with the sequences defined under e),
- g) sequences which include the specific N terminus of the polypeptide shown in SEQ ID NO: 2,
- h) sequences which have an identity of at least 60% with the sequences defined under g).

38. A method according to Claim 37, wherein the polypeptide comprises a sequence selected from the group consisting of:

- a) the sequence shown in SEQ ID NO: 2,
- b) sequences encoded by a nucleic acid having SEQ ID NO: 1,
- c) sequences which include the C-terminally localized active site of the polypeptide shown in SEQ ID NO: 2,
- d) sequences which include the specific N terminus of the polypeptide shown in SEQ ID NO: 2.

39. A method according to Claim 37, comprising the steps of :

- a) providing a labelled substrate of the polypeptide, and
- b) comparing the conversion of the labelled substrate incubated with the polypeptide in the presence of the target compound to

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the conversion of the labelled substrate incubated with the polypeptide in the absence of the target compound.

40. A method according to Claim 37, comprising the steps of :
 - a) providing a labelled ligand of the polypeptide, and
 - b) comparing the binding of the labelled ligand incubated with the polypeptide in the presence of the target compound to the binding of the labelled ligand substrate incubated with the polypeptide in the absence of the target compound.
41. A method according to Claim 15, comprising the step of contacting a host cell comprising a polypeptide of the sequence SEQ ID NO:2 with a chemical compound under conditions which permit the interaction of the chemical compound with the polypeptide.
42. A method according to Claim 41, wherein the host cell is selected from the group consisting of *E. coli* cells, yeast cells, insect cells, mammalian cells and plant cells.
43. A method according to Claim 16, comprising the step of contacting a host cell comprising a polypeptide of the sequence SEQ ID NO:2 with a chemical compound under conditions which permit the interaction of the chemical compound with the polypeptide.
44. A method according to Claim 43, wherein the host cell is selected from the group consisting of *E. coli* cells, yeast cells, insect cells, mammalian cells and plant cells.
45. A method according to Claim 17, wherein the host cell comprises a nucleic acid of the sequence SEQ ID NO:1.
46. A method according to Claim 45, wherein the host cell is selected from the group consisting of *E. coli* cells, yeast cells, insect cells, mammalian cells and plant cells.